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                                                                                                                                                                                                                                                                   241 VHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                    24. VHTECCHGDLLECADDRADLAKYICENGDSISSKLKECCEKPLLEKSHCIAEVENDEMPA 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 161 CAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           421 PILVEVSRNLGKVGSKOCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              481 LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVRHKPRAT 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 LVNRRPCFSALEVDETYVPKEPNAETFTFHADICTLSEKERQIRKQTALVELVKHKPRAT 540
                                                                                                                                                                    61 NCDKSCHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEV 120
                                                                                                                                                                                                                                            121 DVMCTAFHDNEETFLKKYLYEJARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLP 180
                                                                                                                                                                                                                                                                                                                     181 KLDELRDEGKASSAKORIKCASLOKFGERAFRAWAVARLSORPPKAEFAEVSKLVTDLTK 240
                                                             Gaps
                                                                                               1 DAHKSEVAHRFKDLGEENFKALVLIAFAQTLQQCPFEDHVKLVNEVTEFAKTCVADESAE 60
                                                                                                                  DARKSEVARPROLOSENERALVIJAFAGYLOOPPEDHYKLVARVIEFAKTCVADESAE 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; albumin; ischemic state; serum protein; metal ion salt;
perioperative ischemia, ischemiar myocardial infarction;
progressive coronary artery disease.
                      DB 18; Length 585;
                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         541 KEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKKLVAASQAALGL 585
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                   100.0%; Score 3103; DB 1
100.0%; Pred. No. 1e-254;
ive 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Amino acid sequence of a human albumin protein
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                      Ouery Match 100.0
Best Local Similarity 100.1
Matches 585, Conservative
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                                                                                                                                                                    LVNRRPCFSALEVDETYVPREFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKAT 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 DVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLPPAKRYKAAPTECCQAADKAACLLP 180
                      81 KIDELRDEGRASSAKORÎKCASIOKFGERAFKAWAVARISORFPKAEFAEVSKIVTDIJK 240
                                                                                                   181 KIDELKDEGKASSAKORLKCASLOKFGERAFKAMAVARLSORPFRAEFAFVSKLVTDLTF 240
                                                                                                                                                 241 VHTECCHGDLLECADDRADLAKYICENODSISSKLKECCEKPLLEKSHCIAEVENDEMPA 300
                                                                                                                                                                                                                         301 DLPSLAADFVESKDVCKNYABAKDVFLGBFLKEIARRHPDISVVLLLRIAKTYETTLEKC 360
                                                                                                                                                                                                                                            421 PTLYEVSRNIGKYGSKCCKHPEAKRAPCAEDTLSVVLNQLCVLHEKTPVSDRVTKCCTES 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Serum albumin-growth hormone fusion protein - useful to treat growth hormone related diseases, e.g. Down's syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Serum albumin-growth hormone fusion protein; growth hormone;
Cown's syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSA protein sequence related to the growth hormone protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               541 KEOLKAVMDDFNAFVEKCCKADDKETCFAEEGKKLVAASQAALGL 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA020111 standard; Protein; 585 AA.
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585 AA;

N-PSDB; AAK99568

25-JUN-1998; 30-DEC-1995; 19-DEC-1996;

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Unidentified KR99076789-A 15-0CT-1999.

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